

10/567764

1 IAP5 Rec'd PCT/PTO 10 FEB 2006

SEQUENCE LISTING

<110> Flannery, Carl R
Corcoran, Christopher J
Freeman, Bethany A
Racie, Lisa A

<120> RECOMBINANT LUBRICIN MOLECULES AND USES THEREOF

<130> 19003-002US1

<150> PCT/US2004/026508

<151> 2004-08-13

<150> US 60/495,741

<151> 2003-08-14

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<170> PatentIn version 3.3

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<223> Nucleotide sequence of synthetic cDNA cassette-1.

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Ser	Glu	Asn	Gln	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	165	170	175	
Ser	Thr	Ile	Trp	Lys	Ile	Lys	Ser	Ser	Lys	Asn	Ser	Ala	Ala	Asn	Arg	180	185	190	
Glu	Leu	Gln	Lys	Lys	Leu	Lys	Val	Lys	Asp	Asn	Lys	Lys	Asn	Arg	Thr	195	200	205	
Lys	Lys	Lys	Pro	Thr	Pro	Lys	Pro	Pro	Val	Val	Asp	Glu	Ala	Gly	Ser	210	215	220	
Gly	Leu	Asp	Asn	Gly	Asp	Phe	Lys	Val	Thr	Thr	Pro	Asp	Thr	Ser	Thr	225	230	235	240
Thr	Gln	His	Asn	Lys	Val	Ser	Thr	Ser	Pro	Lys	Ile	Thr	Thr	Ala	Lys	245	250	255	
Pro	Ile	Asn	Pro	Arg	Pro	Ser	Leu	Pro	Pro	Asn	Ser	Asp	Thr	Ser	Lys	260	265	270	
Glu	Thr	Ser	Leu	Thr	Val	Asn	Lys	Glu	Thr	Thr	Val	Glu	Thr	Lys	Glu	275	280	285	

Thr	Thr	Thr	Thr	Asn	Lys	Gln	Thr	Ser	Thr	Asp	Gly	Lys	Glu	Lys	Thr	290	295	300	
Thr	Ser	Ala	Lys	Glu	Thr	Gln	Ser	Ile	Glu	Lys	Thr	Ser	Ala	Lys	Asp	305	310	315	320
Leu	Ala	Pro	Thr	Ser	Lys	Val	Leu	Ala	Lys	Pro	Thr	Pro	Lys	Ala	Glu	325	330	335	
Thr	Thr	Thr	Lys	Gly	Pro	Ala	Leu	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro	340	345	350	
Thr	Thr	Pro	Lys	Glu	Pro	Ala	Ser	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro	355	360	365	
Thr	Thr	Ile	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	370	375	380	
Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	385	390	395	400
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr	405	410	415	
Thr	Lys	Pro	Ala	Pro	Thr	Thr	Pro	Glu	Thr	Pro	Pro	Pro	Thr	Thr	Ser	420	425	430	
Glu	Val	Ser	Thr	Pro	Thr	Thr	Thr	Lys	Glu	Pro	Thr	Thr	Ile	His	Lys	435	440	445	
Ser	Pro	Asp	Glu	Ser	Thr	Pro	Glu	Leu	Ser	Ala	Glu	Pro	Thr	Pro	Lys	450	455	460	
Ala	Leu	Glu	Asn	Ser	Pro	Lys	Glu	Pro	Gly	Val	Pro	Thr	Thr	Lys	Thr	465	470	475	480
Pro	Ala	Ala	Thr	Lys	Pro	Glu	Met	Thr	Thr	Thr	Ala	Lys	Asp	Lys	Thr	485	490	495	
Thr	Glu	Arg	Asp	Leu	Arg	Thr	Thr	Pro	Glu	Thr	Thr	Thr	Ala	Ala	Pro	500	505	510	
Lys	Met	Thr	Lys	Glu	Thr	Ala	Thr	Thr	Thr	Glu	Lys	Thr	Thr	Glu	Ser	515	520	525	
Lys	Ile	Thr	Ala	Thr	Thr	Thr	Gln	Val	Thr	Ser	Thr	Thr	Thr	Gln	Asp	530	535	540	
Thr	Thr	Pro	Phe	Lys	Ile	Thr	Thr	Leu	Lys	Thr	Thr	Thr	Leu	Ala	Pro	545	550	555	560
Lys	Val	Thr	Thr	Thr	Lys	Lys	Thr	Ile	Thr	Thr	Thr	Glu	Ile	Met	Asn	565	570	575	
Lys	Pro	Glu	Glu	Thr	Ala	Lys	Pro	Lys	Asp	Arg	Ala	Thr	Asn	Ser	Lys				

580					585					590						
Ala	Thr	Thr	Pro	Lys	Pro	Gln	Lys	Pro	Thr	Lys	Ala	Pro	Lys	Lys	Pro	
595					600					605						
Thr	Ser	Thr	Lys	Lys	Pro	Lys	Thr	Met	Pro	Arg	Val	Arg	Lys	Pro	Lys	
610					615					620						
Thr	Thr	Pro	Thr	Pro	Arg	Lys	Met	Thr	Ser	Thr	Met	Pro	Glu	Leu	Asn	
625					630					635					640	
Pro	Thr	Ser	Arg	Ile	Ala	Glu	Ala	Met	Leu	Gln	Thr	Thr	Thr	Arg	Pro	
645					650					655						
Asn	Gln	Thr	Pro	Asn	Ser	Lys	Leu	Val	Glu	Val	Asn	Pro	Lys	Ser	Glu	
660					665					670						
Asp	Ala	Gly	Gly	Ala	Glu	Gly	Glu	Thr	Pro	His	Met	Leu	Leu	Arg	Pro	
675					680					685						
His	Val	Phe	Met	Pro	Glu	Val	Thr	Pro	Asp	Met	Asp	Tyr	Leu	Pro	Arg	
690					695					700						
Val	Pro	Asn	Gln	Gly	Ile	Ile	Ile	Asn	Pro	Met	Leu	Ser	Asp	Glu	Thr	
705					710					715					720	
Asn	Ile	Cys	Asn	Gly	Lys	Pro	Val	Asp	Gly	Leu	Thr	Thr	Leu	Arg	Asn	
725					730					735						
Gly	Thr	Leu	Val	Ala	Phe	Arg	Gly	His	Tyr	Phe	Trp	Met	Leu	Ser	Pro	
740					745					750						
Phe	Ser	Pro	Pro	Ser	Pro	Ala	Arg	Arg	Ile	Thr	Glu	Val	Trp	Gly	Ile	
755					760					765						
Pro	Ser	Pro	Ile	Asp	Thr	Val	Phe	Thr	Arg	Cys	Asn	Cys	Glu	Gly	Lys	
770					775					780						
Thr	Phe	Phe	Phe	Lys	Asp	Ser	Gln	Tyr	Trp	Arg	Phe	Thr	Asn	Asp	Ile	
785					790					795					800	
Lys	Asp	Ala	Gly	Tyr	Pro	Lys	Pro	Ile	Phe	Lys	Gly	Phe	Gly	Gly	Leu	
805					810					815						
Thr	Gly	Gln	Ile	Val	Ala	Ala	Leu	Ser	Thr	Ala	Lys	Tyr	Lys	Asn	Trp	
820					825					830						
Pro	Glu	Ser	Val	Tyr	Phe	Phe	Lys	Arg	Gly	Gly	Ser	Ile	Gln	Gln	Tyr	
835					840					845						
Ile	Tyr	Lys	Gln	Glu	Pro	Val	Gln	Lys	Cys	Pro	Gly	Arg	Arg	Pro	Ala	
850					855					860						
Leu	Asn	Tyr	Pro	Val	Tyr	Gly	Glu	Met	Thr	Gln	Val	Arg	Arg	Arg	Arg	
865					870					875					880	

Phe Glu Arg Ala Ile Gly Pro Ser Gln Thr His Thr Ile Arg Ile Gln
 885 890 895

Tyr Ser Pro Ala Arg Leu Ala Tyr Gln Asp Lys Gly Val Leu His Asn
 900 905 910

Glu Val Lys Val Ser Ile Leu Trp Arg Gly Leu Pro Asn Val Val Thr
 915 920 925

Ser Ala Ile Ser Leu Pro Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr
 930 935 940

Tyr Ala Phe Ser Lys Asp Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg
 945 950 955 960

Thr Ala Arg Ala Ile Thr Thr Arg Ser Gly Gln Thr Leu Ser Lys Val
 965 970 975

Trp Tyr Asn Cys Pro
 980

<210> 8
 <211> 157
 <212> DNA
 <213> Artificial

<220>
 <223> Lub:1 DNA insert from synthetic cDNA cassette-1.

<400> 8
 gcgcgcccac aactccaaaa gagcccgcac ctaccacgac aaagtcagct cctactacgc 60
 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaggagccag 120
 ctctactac aacgaaaccg gcaccaacca ctccgga 157

<210> 9
 <211> 51
 <212> PRT
 <213> Artificial

<220>
 <223> 51 amino acids encoded by Lub:1 DNA insert (4 KEPAPTT sequences
 between S373 to E425 in SEQ ID NO: 7).

<400> 9

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Pro Ala Pro
 35 40 45

Thr Thr Pro
 50

<210> 10
 <211> 3024
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant PRG4-Lub:2 cDNA construct.

<400> 10
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 caagtttcat ctcaagattt atcaagctgt gcagggagat gtggggaagg gtattctaga 120
 gatgccacct gcaactgtga ttataactgt caacactaca tggagtgctg ccctgatttc 180
 aagagagtct gcactgcgga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgctg tcccgattat 300
 gagagtttct gtgcagaagt gcataatccc acatcaccac catcttcaaa gaaagcacct 360
 ccaccttcag gagcatctca aaccatcaaa tcaacaacca aacgttcacc caaaccacca 420
 aacaagaaga agactaagaa agttatagaa tcagaggaaa taacagaaga acattctgtt 480
 tctgaaaatc aagagtcttc ctccagtagc agttcaagta gttcgtcgtc gacaatttgg 540
 aaaatcaagt cttccaaaaa ttcagctgct aatagagaat tacagaagaa actcaaagta 600
 aaagataaca agaagaacag aactaaaaag aaacctaccc ccaaaccacc agttgtagat 660
 gaagctggaa gtggattgga caatggtgac ttcaaggta caactcctga cacgtctacc 720
 acccaacaca ataaagtcag cacatctccc aagatdaca cagcaaaacc aataaatccc 780
 agaccagtc ttccaccta ttctgataca tctaaagaga cgtctttgac agtgaataaa 840
 gagacaacag ttgaaactaa agaaactact acaacaaata aacagacttc aactgatgga 900
 aaagagaaga ctacttccgc taaagagaca caaagtatag agaaaacatc tgctaaagat 960
 ttagcaccca catctaaagt gctggctaaa cctacacca aagctgaaac tacaaccaa 1020
 ggccctgctc tcaccactcc caaggagccc acgccacca ctccaagga gcctgcatct 1080
 accacacca aagagcccac acctaccacc atcaagagcg cgcccacaac tccaaaagag 1140

ccgcaccta	ccacgacaaa	gtcagctcct	actacgcccc	aagagccagc	gccgacgact	1200
actaaagaac	cggcaccac	cacgcctaaa	gaaccagccc	ctactacgac	aaaggagcct	1260
gcaccacaaa	ccacgaagag	cgcaccacaca	acaccaaagg	agccggcccc	tacgactcct	1320
aaggaaccca	aaccggcacc	aaccactccg	gaaacacctc	ctccaaccac	ttcagaggtc	1380
tctactccaa	ctaccaccaa	ggagcctacc	actatccaca	aaagccctga	tgaatcaact	1440
cctgagcttt	ctgcagaacc	cacaccaaaa	gctcttgaaa	acagtcccaa	ggaacctggt	1500
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aagacaacag	aaagagactt	acgtactaca	cctgaaacta	caactgctgc	acctaagatg	1620
acaaaagaga	cagcaactac	aacagaaaaa	actaccgaat	ccaaaataac	agctacaacc	1680
acacaagtaa	catctaccac	aactcaagat	accacaccat	tcaaaattac	tactcttaaa	1740
acaactactc	ttgcacccaa	agtaactaca	acaaaaaaga	caattactac	cactgagatt	1800
atgaacaaac	ctgaagaaac	agctaaacca	aaagacagag	ctactaattc	taaagcgaca	1860
actcctaaac	ctcaaaagcc	aaccaaagca	ccaaaaaac	ccacttctac	caaaaagcca	1920
aaaacaatgc	ctagagtgcg	aaaaccaaag	acgacaccaa	ctccccgcaa	gatgacatca	1980
acaatgccag	aattgaaccc	tacctcaaga	atagcagaag	ccatgctcca	aaccaccacc	2040
agacctaac	aaactccaaa	ctccaaacta	gttgaagtaa	atccaaagag	tgaagatgca	2100
gggtggtgctg	aaggagaaac	acctcatatg	cttctcaggc	cccatgtggt	catgcctgaa	2160
gttactcccg	acatggatta	cttaccgaga	gtaccaatc	aaggcattat	catcaatccc	2220
atgctttccg	atgagaccaa	tatatgcaat	ggtaagccag	tagatggact	gactactttg	2280
cgcaatggga	cattagttgc	attccgaggt	cattatctct	ggatgctaag	tccattcagt	2340
ccaccatctc	cagctcgag	aattactgaa	gtttggggta	ttccttcccc	cattgatact	2400
gtttttacta	ggtgcaactg	tgaaggaaaa	actttcttct	ttaaggattc	tcagtactgg	2460
cgttttacca	atgatataaa	agatgcaggg	taccccaaac	caattttcaa	aggatttgga	2520
ggactaactg	gacaaatagt	ggcagcgctt	tcaacagcta	aatataagaa	ctggcctgaa	2580
tctgtgtatt	ttttcaagag	aggtggcagc	attcagcagt	atatttataa	acaggaacct	2640
gtacagaagt	gccctggaag	aaggcctgct	ctaaattatc	cagtgtatgg	agaaatgaca	2700
caggtagga	gacgtcgctt	tgaacgtgct	ataggacctt	ctcaaacaca	caccatcaga	2760
attcaatatt	cacctgccag	actggcttat	caagacaaag	gtgtccttca	taatgaagtt	2820

aaagtgagta tactgtggag aggacttcca aatgtgggta cctcagctat atcactgccc 2880
 aacatcagaa aacctgacgg ctatgattac tatgcctttt ctaaagatca atactataac 2940
 attgatgtgc ctagtagaac agcaagagca attactactc gttctgggca gaccttatcc 3000
 aaagtctggt acaactgtcc ttaa 3024

<210> 11
 <211> 1007
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence of entire PRG4-LUB:2 protein.

<400> 11

Met	Ala	Trp	Lys	Thr	Leu	Pro	Ile	Tyr	Leu	Leu	Leu	Leu	Leu	Ser	Val	1	5	10	15
Phe	Val	Ile	Gln	Gln	Val	Ser	Ser	Gln	Asp	Leu	Ser	Ser	Cys	Ala	Gly	20	25	30	
Arg	Cys	Gly	Glu	Gly	Tyr	Ser	Arg	Asp	Ala	Thr	Cys	Asn	Cys	Asp	Tyr	35	40	45	
Asn	Cys	Gln	His	Tyr	Met	Glu	Cys	Cys	Pro	Asp	Phe	Lys	Arg	Val	Cys	50	55	60	
Thr	Ala	Glu	Leu	Ser	Cys	Lys	Gly	Arg	Cys	Phe	Glu	Ser	Phe	Glu	Arg	65	70	75	80
Gly	Arg	Glu	Cys	Asp	Cys	Asp	Ala	Gln	Cys	Lys	Lys	Tyr	Asp	Lys	Cys	85	90	95	
Cys	Pro	Asp	Tyr	Glu	Ser	Phe	Cys	Ala	Glu	Val	His	Asn	Pro	Thr	Ser	100	105	110	
Pro	Pro	Ser	Ser	Lys	Lys	Ala	Pro	Pro	Pro	Ser	Gly	Ala	Ser	Gln	Thr	115	120	125	
Ile	Lys	Ser	Thr	Thr	Lys	Arg	Ser	Pro	Lys	Pro	Pro	Asn	Lys	Lys	Lys	130	135	140	
Thr	Lys	Lys	Val	Ile	Glu	Ser	Glu	Glu	Ile	Thr	Glu	Glu	His	Ser	Val	145	150	155	160
Ser	Glu	Asn	Gln	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	165	170	175	
Ser	Thr	Ile	Trp	Lys	Ile	Lys	Ser	Ser	Lys	Asn	Ser	Ala	Ala	Asn	Arg	180	185	190	

Glu	Leu	Gln	Lys	Lys	Leu	Lys	Val	Lys	Asp	Asn	Lys	Lys	Asn	Arg	Thr
195						200				205					
Lys	Lys	Lys	Pro	Thr	Pro	Lys	Pro	Pro	Val	Val	Asp	Glu	Ala	Gly	Ser
210						215				220					
Gly	Leu	Asp	Asn	Gly	Asp	Phe	Lys	Val	Thr	Thr	Pro	Asp	Thr	Ser	Thr
225				230						235		240			
Thr	Gln	His	Asn	Lys	Val	Ser	Thr	Ser	Pro	Lys	Ile	Thr	Thr	Ala	Lys
				245				250						255	
Pro	Ile	Asn	Pro	Arg	Pro	Ser	Leu	Pro	Pro	Asn	Ser	Asp	Thr	Ser	Lys
		260						265				270			
Glu	Thr	Ser	Leu	Thr	Val	Asn	Lys	Glu	Thr	Thr	Val	Glu	Thr	Lys	Glu
275						280						285			
Thr	Thr	Thr	Thr	Asn	Lys	Gln	Thr	Ser	Thr	Asp	Gly	Lys	Glu	Lys	Thr
290						295				300					
Thr	Ser	Ala	Lys	Glu	Thr	Gln	Ser	Ile	Glu	Lys	Thr	Ser	Ala	Lys	Asp
305				310						315				320	
Leu	Ala	Pro	Thr	Ser	Lys	Val	Leu	Ala	Lys	Pro	Thr	Pro	Lys	Ala	Glu
				325				330						335	
Thr	Thr	Thr	Lys	Gly	Pro	Ala	Leu	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro
		340				345						350			
Thr	Thr	Pro	Lys	Glu	Pro	Ala	Ser	Thr	Thr	Pro	Lys	Glu	Pro	Thr	Pro
355						360						365			
Thr	Thr	Ile	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr
370						375				380					
Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr
385				390						395		400			
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Ala	Pro	Thr	Thr
				405				410						415	
Thr	Lys	Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro
		420						425				430			
Lys	Glu	Pro	Ala	Pro	Thr	Thr	Pro	Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr
435						440				445					
Thr	Pro	Glu	Thr	Pro	Pro	Pro	Thr	Thr	Ser	Glu	Val	Ser	Thr	Pro	Thr
450						455				460					
Thr	Thr	Lys	Glu	Pro	Thr	Thr	Ile	His	Lys	Ser	Pro	Asp	Glu	Ser	Thr
465				470						475		480			

Pro Glu Leu Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro
 485 490 495
 Lys Glu Pro Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro
 500 505 510
 Glu Met Thr Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg
 515 520 525
 Thr Thr Pro Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr
 530 535 540
 Ala Thr Thr Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr
 545 550 555 560
 Thr Gln Val Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile
 565 570 575
 Thr Thr Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys
 580 585 590
 Lys Thr Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala
 595 600 605
 Lys Pro Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro
 610 615 620
 Gln Lys Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro
 625 630 635 640
 Lys Thr Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg
 645 650 655
 Lys Met Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala
 660 665 670
 Glu Ala Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser
 675 680 685
 Lys Leu Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu
 690 695 700
 Gly Glu Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu
 705 710 715 720
 Val Thr Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile
 725 730 735
 Ile Ile Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys
 740 745 750
 Pro Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe
 755 760 765
 Arg Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro

770	775	780
Ala Arg Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr		
785	790	795 800
Val Phe Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp		
	805	810 815
Ser Gln Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro		
	820	825 830
Lys Pro Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala		
	835	840 845
Ala Leu Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe		
	850	855 860
Phe Lys Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro		
	865	870 875 880
Val Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr		
	885	890 895
Gly Glu Met Thr Gln Val Arg Arg Arg Arg Phe Glu Arg Ala Ile Gly		
	900	905 910
Pro Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu		
	915	920 925
Ala Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile		
	930	935 940
Leu Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro		
	945	950 955 960
Asn Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp		
	965	970 975
Gln Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr		
	980	985 990
Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro		
	995	1000 1005
<210> 12		
<211> 235		
<212> DNA		
<213> Artificial		
<220>		
<223> Lub:2 DNA insert from synthetic cDNA cassette-1 and one synthetic cDNA cassette-2 sequence.		
<400> 12		

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 ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag 120
 cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa 180
 aggagccggc ccctacgact cctaaggaac ccaaaccggc accaaccact ccgga 235

<210> 13
 <211> 77
 <212> PRT
 <213> Artificial

<220>
 <223> 77 amino acids encoded by Lub:2 DNA insert (6 KEPAPTT sequences between S373 and E451 in SEQ ID NO: 11).

<400> 13

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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 65 70 75

<210> 14
 <211> 3117
 <212> DNA
 <213> Artificial

<220>
 <223> Recombinant PRG4-Lub:3 cDNA construct.

<400> 14

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 gatgccacct gcaactgtga ttataactgt caacactaca tggagtgcct ccctgatttc 180
 aagagagtct gcaactgcga gctttcctgt aaaggccgct gctttgagtc cttcgagaga 240
 gggagggagt gtgactgcga cgcccaatgt aagaagtatg acaagtgcct tcccatttat 300

gagagtttct	gtgcagaagt	gcataatccc	acatcaccac	catcttcaaa	gaaagcacct	360
ccaccttcag	gagcatctca	aaccatcaaa	tcaacaacca	aacgttcacc	caaaccacca	420
aacaagaaga	agactaagaa	agttatagaa	tcagaggaaa	taacagaaga	acattctggt	480
tctgaaaatc	aagagtccct	ctccagtagc	agttcaagta	gttcgctcgtc	gacaatttgg	540
aaaatcaagt	cttccaaaaa	ttcagctgct	aatagagaat	tacagaagaa	actcaaagta	600
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<210> 15

<211> 1038

<212> PRT

<213> Artificial

<220>

<223> amino acid sequence of entire PRG4-LUB:3 protein

<400> 15

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Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
          20           25           30

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Gly	Arg	Glu	Cys	Asp	Cys	Asp	Ala	Gln	Cys	Lys	Lys	Tyr	Asp	Lys	Cys	85	90	95	
Cys	Pro	Asp	Tyr	Glu	Ser	Phe	Cys	Ala	Glu	Val	His	Asn	Pro	Thr	Ser	100	105	110	
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Ser	Glu	Asn	Gln	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	165	170	175	
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Lys	Lys	Lys	Pro	Thr	Pro	Lys	Pro	Pro	Val	Val	Asp	Glu	Ala	Gly	Ser	210	215	220	
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Pro	Ile	Asn	Pro	Arg	Pro	Ser	Leu	Pro	Pro	Asn	Ser	Asp	Thr	Ser	Lys	260	265	270	
Glu	Thr	Ser	Leu	Thr	Val	Asn	Lys	Glu	Thr	Thr	Val	Glu	Thr	Lys	Glu	275	280	285	
Thr	Thr	Thr	Thr	Asn	Lys	Gln	Thr	Ser	Thr	Asp	Gly	Lys	Glu	Lys	Thr	290	295	300	
Thr	Ser	Ala	Lys	Glu	Thr	Gln	Ser	Ile	Glu	Lys	Thr	Ser	Ala	Lys	Asp	305	310	315	320

Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
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 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
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 355 360 365
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 450 455 460
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 465 470 475 480
 Pro Glu Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr
 485 490 495
 Thr Lys Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro
 500 505 510
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Leu	Val	Glu	Val	Asn	Pro	Lys	Ser	Glu	Asp	Ala	Gly	Gly	Ala	Glu	Gly
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Glu	Thr	Pro	His	Met	Leu	Leu	Arg	Pro	His	Val	Phe	Met	Pro	Glu	Val
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		755					760					765			
Ile	Asn	Pro	Met	Leu	Ser	Asp	Glu	Thr	Asn	Ile	Cys	Asn	Gly	Lys	Pro
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Gly	His	Tyr	Phe	Trp	Met	Leu	Ser	Pro	Phe	Ser	Pro	Pro	Ser	Pro	Ala
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Arg	Arg	Ile	Thr	Glu	Val	Trp	Gly	Ile	Pro	Ser	Pro	Ile	Asp	Thr	Val
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Phe	Thr	Arg	Cys	Asn	Cys	Glu	Gly	Lys	Thr	Phe	Phe	Phe	Lys	Asp	Ser
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Gln	Tyr	Trp	Arg	Phe	Thr	Asn	Asp	Ile	Lys	Asp	Ala	Gly	Tyr	Pro	Lys
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Leu	Ser	Thr	Ala	Lys	Tyr	Lys	Asn	Trp	Pro	Glu	Ser	Val	Tyr	Phe	Phe
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			900					905					910		

Gln Lys Cys Pro Gly Arg Arg Pro Ala Leu Asn Tyr Pro Val Tyr Gly
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Glu Met Thr Gln Val Arg Arg Arg Phe Glu Arg Ala Ile Gly Pro
 930 935 940

Ser Gln Thr His Thr Ile Arg Ile Gln Tyr Ser Pro Ala Arg Leu Ala
 945 950 955 960

Tyr Gln Asp Lys Gly Val Leu His Asn Glu Val Lys Val Ser Ile Leu
 965 970 975

Trp Arg Gly Leu Pro Asn Val Val Thr Ser Ala Ile Ser Leu Pro Asn
 980 985 990

Ile Arg Lys Pro Asp Gly Tyr Asp Tyr Tyr Ala Phe Ser Lys Asp Gln
 995 1000 1005

Tyr Tyr Asn Ile Asp Val Pro Ser Arg Thr Ala Arg Ala Ile Thr
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Thr Arg Ser Gly Gln Thr Leu Ser Lys Val Trp Tyr Asn Cys Pro
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<210> 16

<211> 328

<212> DNA

<213> Artificial

<220>

<223> Lub:3 DNA insert from synthetic cDNA cassette-1 and two synthetic cDNA cassette-2 sequences.

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 aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac 240
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<210> 17

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 108 amino acids encoded by Lub:3 DNA insert (9 KEPAPTT sequences between S373 and E482 in SEQ ID NO: 15)

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Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
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Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
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<210> 18

<211> 3210

<212> DNA

<213> Artificial

<220>

<223> recombinant PRG4-Lub:4 cDNA construct.

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<210> 19

<211> 1069

<212> PRT

<213> Artificial

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<223> amino acid sequence of entire PRG4-LUB:4 protein.

<400> 19

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Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
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Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
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Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys

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Cys	Pro	Asp	Tyr	Glu	Ser	Phe	Cys	Ala	Glu	Val	His	Asn	Pro	Thr	Ser
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Pro	Pro	Ser	Ser	Lys	Lys	Ala	Pro	Pro	Pro	Ser	Gly	Ala	Ser	Gln	Thr
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Ile	Lys	Ser	Thr	Thr	Lys	Arg	Ser	Pro	Lys	Pro	Pro	Asn	Lys	Lys	Lys
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Lys	Lys	Lys	Pro	Thr	Pro	Lys	Pro	Pro	Val	Val	Asp	Glu	Ala	Gly	Ser
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Pro	Ile	Asn	Pro	Arg	Pro	Ser	Leu	Pro	Pro	Asn	Ser	Asp	Thr	Ser	Lys
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 625 630 635 640

Leu Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr
 645 650 655
 Ile Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro
 660 665 670
 Lys Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys
 675 680 685
 Pro Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr
 690 695 700
 Met Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met
 705 710 715 720
 Thr Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala
 725 730 735
 Met Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu
 740 745 750
 Val Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu
 755 760 765
 Thr Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr
 770 775 780
 Pro Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile
 785 790 795 800
 Asn Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val
 805 810 815
 Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg Gly
 820 825 830
 His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala Arg
 835 840 845
 Arg Ile Thr Glu Val Trp Gly Ile Pro Ser Pro Ile Asp Thr Val Phe
 850 855 860
 Thr Arg Cys Asn Cys Glu Gly Lys Thr Phe Phe Phe Lys Asp Ser Gln
 865 870 875 880
 Tyr Trp Arg Phe Thr Asn Asp Ile Lys Asp Ala Gly Tyr Pro Lys Pro
 885 890 895
 Ile Phe Lys Gly Phe Gly Gly Leu Thr Gly Gln Ile Val Ala Ala Leu
 900 905 910
 Ser Thr Ala Lys Tyr Lys Asn Trp Pro Glu Ser Val Tyr Phe Phe Lys
 915 920 925
 Arg Gly Gly Ser Ile Gln Gln Tyr Ile Tyr Lys Gln Glu Pro Val Gln

<210>	20
<211>	421
<212>	DNA
<213>	Artificial

<223> Lub:4 DNA insert from cDNA cassette-1 and three synthetic cDNA cassette-2 sequences.

gcgcgccac	aactccaaaa	gagcccgac	ctaccacgac	aaagtcagct	cctactacgc	60
ccaaagagcc	agcgccgacg	actactaaag	aaccggcacc	caccacgcct	aaagaaccag	120
cccctactac	gacaaaggag	cctgcaccca	caaccacgaa	gagcgcaccc	acaacaccaa	180
aggagccggc	ccctacgact	cctaaagaac	cagcccctac	tacgacaaag	gagcctgcac	240
ccacaaccac	gaagagcgca	cccacaacac	caaaggagcc	ggcccctacg	actcctaaag	300
aaccagcccc	tactacgaca	aaggagcctg	caccacaaac	cacgaagagc	gcaccacaaa	360
caccaaagga	gccggcccct	acgactccta	aggaacccaa	accggcacca	accactccgg	420

a 421

<210> 21
 <211> 139
 <212> PRT
 <213> Artificial

<220>

<223> 139 amino acids encoded by Lub:4 DNA insert (12 KEPAPTT sequences between S373 and E513 in SEQ ID NO: 19)

<400> 21

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 35 40 45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
 50 55 60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
 65 70 75 80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 85 90 95

Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
 100 105 110

Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 115 120 125

Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 130 135

<210> 22
 <211> 3303
 <212> DNA
 <213> Artificial

<220>

<223> Recombinant PRG4-Lub:5 cDNA construct

<400> 22

atggcatgga aaacacttcc catttacctg ttgttgctgc tgtctgtttt cgtgattcag 60

caagtttcat ctcaagattt atcaagctgt gcaggagat gtggggaagg gtattctaga 120

gatgccacct gcaactgtga ttataactgt caacactaca tggagtgtg ccctgatttc 180

aagagagtct	gcactgcgga	gctttcctgt	aaaggccgct	gctttgagtc	cttcgagaga	240
gggagggagt	gtgactgcga	cgcccaatgt	aagaagtatg	acaagtgctg	tcccgattat	300
gagagtttct	gtgcagaagt	gcataatccc	acatcaccac	catcttcaaa	gaaagcacct	360
ccaccttcag	gagcatctca	aaccatcaaa	tcaacaacca	aacgttcacc	caaaccacca	420
aacaagaaga	agactaagaa	agttatagaa	tcagaggaaa	taacagaaga	acattctgtt	480
tctgaaaatc	aagagtcttc	ctccagtagc	agttcaagta	gttcgtcgtc	gacaatttgg	540
aaaatcaagt	cttccaaaaa	ttcagctgct	aatagagaat	tacagaagaa	actcaaagta	600
aaagataaca	agaagaacag	aactaaaaag	aaacctaccc	ccaaaccacc	agttgtagat	660
gaagctggaa	gtggattgga	caatggtgac	ttcaagggtca	caactcctga	cacgtctacc	720
acccaacaca	ataaagtcag	cacatctccc	aagatcacia	cagcaaaacc	aataaatccc	780
agaccagtc	ttccacctaa	ttctgatata	tctaaagaga	cgtctttgac	agtgaataaa	840
gagacaacag	ttgaaactaa	agaaactact	acaacaaata	aacagacttc	aactgatgga	900
aaagagaaga	ctacttccgc	taaagagaca	caaagtatag	agaaaacatc	tgctaaagat	960
ttagcaccca	catctaaagt	gctggctaaa	cctacaccca	aagctgaaac	tacaaccaaa	1020
ggccctgctc	tcaccactcc	caaggagccc	acgcccacca	ctcccaagga	gcctgcatct	1080
accacaccca	aagagcccac	acctaccacc	atcaagagcg	cgcccacaac	tccaaaagag	1140
cccgcacctc	ccacgacaaa	gtcagctcct	actacgcccc	aagagccagc	gccgacgact	1200
actaaagaac	cggcaccac	cacgcctaaa	gaaccagccc	ctactacgac	aaaggagcct	1260
gcaccacaaa	ccacgaagag	cgcaccaca	acaccaaagg	agccggcccc	tacgactcct	1320
aaagaaccag	cccctactac	gacaaaggag	cctgcaccca	caaccacgaa	gagcgacccc	1380
acaacaccaa	aggagccggc	ccctacgact	cctaaagaac	cagcccctac	tacgacaaag	1440
gagcctgcac	ccacaaccac	gaagagcgca	cccacaacac	caaaggagcc	ggcccctacg	1500
actcctaaag	aaccagcccc	tactacgaca	aaggagcctg	caccacaaac	cacgaagagc	1560
gcaccacaaa	caccaaagga	gccggcccct	acgactccta	aggaacccaa	accggcacca	1620
accactccgg	aaacacctcc	tccaaccact	tcagaggtct	ctactccaac	taccaccaag	1680
gagcctacca	ctatccacaa	aagccctgat	gaatcaactc	ctgagctttc	tgcagaaccc	1740
acaccaaaaag	ctcttgaaaa	cagtcccaag	gaacctggtg	tacctacaac	taagacgccg	1800

gcggcgacta aacctgaaat gactacaaca gctaaagaca agacaacaga aagagactta	1860
cgtactacac ctgaaactac aactgctgca cctaagatga caaaagagac agcaactaca	1920
acagaaaaaa ctaccgaatc caaaataaca gctacaacca cacaagtaac atctaccaca	1980
actcaagata ccacaccatt caaaattact actcttaaaa caactactct tgcacccaaa	2040
gtaactacaa caaaaaagac aattactacc actgagatta tgaacaaacc tgaagaaaca	2100
gctaaaccaa aagacagagc tactaattct aaagcgacaa ctcttaaacc tcaaaagcca	2160
accaaagcac ccaaaaaacc cacttctacc aaaaagccaa aaacaatgcc tagagtgaga	2220
aaaccaaaga cgacaccaac tccccgcaag atgacatcaa caatgccaga attgaaccct	2280
acctcaagaa tagcagaagc catgctccaa accaccacca gacctaacca aactccaaac	2340
tccaaactag ttgaagtaaa tccaaagagt gaagatgcag gtggtgctga aggagaaaca	2400
cctcatatgc ttctcaggcc ccatgtgttc atgcctgaag ttactccga catggattac	2460
ttaccgagag tacccaatca aggcattatc atcaatccca tgctttccga tgagaccaat	2520
atatgcaatg gtaagccagt agatggactg actactttgc gcaatgggac attagttgca	2580
ttccgaggtc attatttctg gatgctaagt ccattcagtc caccatctcc agctcgcaga	2640
attactgaag tttggggtat tccttcccc attgatactg tttttactag gtgcaactgt	2700
gaaggaaaaa ctttcttctt taaggattct cagtactggc gttttaccaa tgatataaaa	2760
gatgcagggg accccaaacc aattttcaaa ggatttggag gactaactgg acaaatagtg	2820
gcagcgcttt caacagctaa atataagaac tggcctgaat ctgtgtattt tttcaagaga	2880
ggtggcagca ttcagcagta tatttataaa caggaacctg tacagaagtg ccctggaaga	2940
aggcctgctc taaattatcc agtgtatgga gaaatgacac aggttaggag acgtcgcttt	3000
gaacgtgcta taggaccttc tcaaacacac accatcagaa ttcaatattc acctgccaga	3060
ctggcttatc aagacaaagg tgtccttcat aatgaagtta aagtgagtat actgtggaga	3120
ggacttccaa atgtgggttac ctcagctata tctactgcca acatcagaaa acctgacggc	3180
tatgattact atgccttttc taaagatcaa tactataaca ttgatgtgcc tagtagaaca	3240
gcaagagcaa ttactactcg ttctgggcag accttatcca aagtctggta caactgtcct	3300
taa	3303

<210> 23

<211> 1100

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence of entire PRG4-LUB:5 protein.

<400> 23

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Phe Val Ile Gln Gln Val Ser Ser Gln Asp Leu Ser Ser Cys Ala Gly
          20           25           30

Arg Cys Gly Glu Gly Tyr Ser Arg Asp Ala Thr Cys Asn Cys Asp Tyr
          35           40           45

Asn Cys Gln His Tyr Met Glu Cys Cys Pro Asp Phe Lys Arg Val Cys
          50           55           60

Thr Ala Glu Leu Ser Cys Lys Gly Arg Cys Phe Glu Ser Phe Glu Arg
65           70           75           80

Gly Arg Glu Cys Asp Cys Asp Ala Gln Cys Lys Lys Tyr Asp Lys Cys
          85           90           95

Cys Pro Asp Tyr Glu Ser Phe Cys Ala Glu Val His Asn Pro Thr Ser
          100          105          110

Pro Pro Ser Ser Lys Lys Ala Pro Pro Pro Ser Gly Ala Ser Gln Thr
          115          120          125

Ile Lys Ser Thr Thr Lys Arg Ser Pro Lys Pro Pro Asn Lys Lys Lys
          130          135          140

Thr Lys Lys Val Ile Glu Ser Glu Glu Ile Thr Glu Glu His Ser Val
145          150          155          160

Ser Glu Asn Gln Glu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
          165          170          175

Ser Thr Ile Trp Lys Ile Lys Ser Ser Lys Asn Ser Ala Ala Asn Arg
          180          185          190

Glu Leu Gln Lys Lys Leu Lys Val Lys Asp Asn Lys Lys Asn Arg Thr
          195          200          205

Lys Lys Lys Pro Thr Pro Lys Pro Pro Val Val Asp Glu Ala Gly Ser
          210          215          220

Gly Leu Asp Asn Gly Asp Phe Lys Val Thr Thr Pro Asp Thr Ser Thr
225          230          235          240

Thr Gln His Asn Lys Val Ser Thr Ser Pro Lys Ile Thr Thr Ala Lys
          245          250          255

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Pro Ile Asn Pro Arg Pro Ser Leu Pro Pro Asn Ser Asp Thr Ser Lys
 260 265 270
 Glu Thr Ser Leu Thr Val Asn Lys Glu Thr Thr Val Glu Thr Lys Glu
 275 280 285
 Thr Thr Thr Thr Asn Lys Gln Thr Ser Thr Asp Gly Lys Glu Lys Thr
 290 295 300
 Thr Ser Ala Lys Glu Thr Gln Ser Ile Glu Lys Thr Ser Ala Lys Asp
 305 310 315 320
 Leu Ala Pro Thr Ser Lys Val Leu Ala Lys Pro Thr Pro Lys Ala Glu
 325 330 335
 Thr Thr Thr Lys Gly Pro Ala Leu Thr Thr Pro Lys Glu Pro Thr Pro
 340 345 350
 Thr Thr Pro Lys Glu Pro Ala Ser Thr Thr Pro Lys Glu Pro Thr Pro
 355 360 365
 Thr Thr Ile Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
 370 375 380
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 385 390 395 400
 Thr Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 405 410 415
 Thr Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro
 420 425 430
 Lys Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr
 435 440 445
 Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys
 450 455 460
 Glu Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
 465 470 475 480
 Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu
 485 490 495
 Pro Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu
 500 505 510
 Pro Ala Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro
 515 520 525
 Ala Pro Thr Thr Pro Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro Glu
 530 535 540

Thr Pro Pro Pro Thr Thr Ser Glu Val Ser Thr Pro Thr Thr Thr Lys
 545 550 555 560
 Glu Pro Thr Thr Ile His Lys Ser Pro Asp Glu Ser Thr Pro Glu Leu
 565 570 575
 Ser Ala Glu Pro Thr Pro Lys Ala Leu Glu Asn Ser Pro Lys Glu Pro
 580 585 590
 Gly Val Pro Thr Thr Lys Thr Pro Ala Ala Thr Lys Pro Glu Met Thr
 595 600 605
 Thr Thr Ala Lys Asp Lys Thr Thr Glu Arg Asp Leu Arg Thr Thr Pro
 610 615 620
 Glu Thr Thr Thr Ala Ala Pro Lys Met Thr Lys Glu Thr Ala Thr Thr
 625 630 635 640
 Thr Glu Lys Thr Thr Glu Ser Lys Ile Thr Ala Thr Thr Thr Gln Val
 645 650 655
 Thr Ser Thr Thr Thr Gln Asp Thr Thr Pro Phe Lys Ile Thr Thr Leu
 660 665 670
 Lys Thr Thr Thr Leu Ala Pro Lys Val Thr Thr Thr Lys Lys Thr Ile
 675 680 685
 Thr Thr Thr Glu Ile Met Asn Lys Pro Glu Glu Thr Ala Lys Pro Lys
 690 695 700
 Asp Arg Ala Thr Asn Ser Lys Ala Thr Thr Pro Lys Pro Gln Lys Pro
 705 710 715 720
 Thr Lys Ala Pro Lys Lys Pro Thr Ser Thr Lys Lys Pro Lys Thr Met
 725 730 735
 Pro Arg Val Arg Lys Pro Lys Thr Thr Pro Thr Pro Arg Lys Met Thr
 740 745 750
 Ser Thr Met Pro Glu Leu Asn Pro Thr Ser Arg Ile Ala Glu Ala Met
 755 760 765
 Leu Gln Thr Thr Thr Arg Pro Asn Gln Thr Pro Asn Ser Lys Leu Val
 770 775 780
 Glu Val Asn Pro Lys Ser Glu Asp Ala Gly Gly Ala Glu Gly Glu Thr
 785 790 795 800
 Pro His Met Leu Leu Arg Pro His Val Phe Met Pro Glu Val Thr Pro
 805 810 815
 Asp Met Asp Tyr Leu Pro Arg Val Pro Asn Gln Gly Ile Ile Ile Asn
 820 825 830
 Pro Met Leu Ser Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro Val Asp

835					840					845					
Gly	Leu	Thr	Thr	Leu	Arg	Asn	Gly	Thr	Leu	Val	Ala	Phe	Arg	Gly	His
850						855					860				
Tyr	Phe	Trp	Met	Leu	Ser	Pro	Phe	Ser	Pro	Pro	Ser	Pro	Ala	Arg	Arg
865						870					875				880
Ile	Thr	Glu	Val	Trp	Gly	Ile	Pro	Ser	Pro	Ile	Asp	Thr	Val	Phe	Thr
				885					890					895	
Arg	Cys	Asn	Cys	Glu	Gly	Lys	Thr	Phe	Phe	Phe	Lys	Asp	Ser	Gln	Tyr
			900					905						910	
Trp	Arg	Phe	Thr	Asn	Asp	Ile	Lys	Asp	Ala	Gly	Tyr	Pro	Lys	Pro	Ile
		915					920					925			
Phe	Lys	Gly	Phe	Gly	Gly	Leu	Thr	Gly	Gln	Ile	Val	Ala	Ala	Leu	Ser
	930					935					940				
Thr	Ala	Lys	Tyr	Lys	Asn	Trp	Pro	Glu	Ser	Val	Tyr	Phe	Phe	Lys	Arg
945						950					955				960
Gly	Gly	Ser	Ile	Gln	Gln	Tyr	Ile	Tyr	Lys	Gln	Glu	Pro	Val	Gln	Lys
			965						970					975	
Cys	Pro	Gly	Arg	Arg	Pro	Ala	Leu	Asn	Tyr	Pro	Val	Tyr	Gly	Glu	Met
			980					985					990		
Thr	Gln	Val	Arg	Arg	Arg	Arg	Phe	Glu	Arg	Ala	Ile	Gly	Pro	Ser	Gln
		995					1000					1005			
Thr	His	Thr	Ile	Arg	Ile	Gln	Tyr	Ser	Pro	Ala	Arg	Leu	Ala	Tyr	
	1010					1015					1020				
Gln	Asp	Lys	Gly	Val	Leu	His	Asn	Glu	Val	Lys	Val	Ser	Ile	Leu	
	1025					1030					1035				
Trp	Arg	Gly	Leu	Pro	Asn	Val	Val	Thr	Ser	Ala	Ile	Ser	Leu	Pro	
	1040					1045					1050				
Asn	Ile	Arg	Lys	Pro	Asp	Gly	Tyr	Asp	Tyr	Tyr	Ala	Phe	Ser	Lys	
	1055					1060					1065				
Asp	Gln	Tyr	Tyr	Asn	Ile	Asp	Val	Pro	Ser	Arg	Thr	Ala	Arg	Ala	
	1070					1075					1080				
Ile	Thr	Thr	Arg	Ser	Gly	Gln	Thr	Leu	Ser	Lys	Val	Trp	Tyr	Asn	
	1085					1090					1095				
Cys	Pro														
	1100														

<211> 514
 <212> DNA
 <213> Artificial

<220>

<223> Lub:5 DNA insert from cDNA cassette-1 and four synthetic cDNA cassette-2 sequences

<400> 24

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ccaaagagcc agcgccgacg actactaaag aaccggcacc caccacgcct aaagaaccag      120
cccctactac gacaaaggag cctgcaccca caaccacgaa gagcgcaccc acaacaccaa      180
aggagccggc ccctacgact cctaaagaac cagcccctac tacgacaaag gagcctgcac      240
ccacaaccac gaagagcgca ccacaacac caaaggagcc ggcccctacg actcctaaag      300
aaccagcccc tactacgaca aaggagcctg caccacaaac cacgaagagc gcacccacaa      360
caccaaagga gccggcccct acgactccta aagaaccagc ccctactacg acaaaggagc      420
ctgcacccac aaccacgaag agcgcaccca caacaccaaa ggagccggcc cctacgactc      480
ctaaggaacc caaaccggca ccaaccactc cgga                                     514
  
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<210> 25
 <211> 170
 <212> PRT
 <213> Artificial

<220>

<223> 170 amino acids encoded by Lub:5 DNA insert (15 KEPAPTT sequences between S373 and E544 in SEQ ID NO: 23)

<400> 25

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Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
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Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
              20              25              30

Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
              35              40              45

Pro Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro
              50              55              60

Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro
65              70              75              80

Thr Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr
  
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85 90 95
 Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr
 100 105 110
 Thr Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr
 115 120 125
 Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr
 130 135 140
 Thr Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro
 145 150 155 160
 Lys Glu Pro Lys Pro Ala Pro Thr Thr Pro
 165 170

<210> 26
 <211> 45
 <212> PRT
 <213> Artificial

<220>
 <223> amino acid sequence "APTTTPKEPAPTTTTSAPTTTPKEPAPTTT
 KEPAPTTTPKEPAPTTTK" (45 amino acids) in preferred PRG4-LUB:N
 protein

<400> 26

Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Ser Ala
 1 5 10 15
 Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala
 20 25 30
 Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Thr Lys
 35 40 45

<210> 27
 <211> 31
 <212> PRT
 <213> Artificial

<220>
 <223> amino acid sequence "KEPAPTTTKEPAPTTTTSAPTTTPKEPAPTTTP" (31 amino
 acids) repeated N-1 times in preferred PRG4-LUB:N protein

<400> 27

Lys Glu Pro Ala Pro Thr Thr Thr Lys Glu Pro Ala Pro Thr Thr Thr
 1 5 10 15
 Lys Ser Ala Pro Thr Thr Pro Lys Glu Pro Ala Pro Thr Thr Pro

20

25

30

<210> 28

<211> 22

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "EPAPTTTKSAPTTPKEPAPTTP" (22 amino acids) joining SEQ ID NO: 26 to (N-2) repeats of SEQ ID NO: 27 in preferred PRG4-LUB:N protein where N = 3 or more.

<400> 28

Glu	Pro	Ala	Pro	Thr	Thr	Thr	Lys	Ser	Ala	Pro	Thr	Thr	Pro	Lys	Glu
1				5					10					15	

Pro	Ala	Pro	Thr	Thr	Pro
					20

<210> 29

<211> 10

<212> PRT

<213> Artificial

<220>

<223> Amino acid sequence "KEPKPAPTTP" (10 amino acids) in preferred PRG4-LUB:N protein where N = 2 or more.

<400> 29

Lys	Glu	Pro	Lys	Pro	Ala	Pro	Thr	Thr	Pro
1				5					10